

Yu-Dong Cai

List of Publications by Year in descending order

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348
papers

14,188
citations

18887

64
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38517

99
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353
all docs

353
docs citations

353
times ranked

8766
citing authors

#	ARTICLE	IF	CITATIONS
1	Using Functional Domain Composition and Support Vector Machines for Prediction of Protein Subcellular Location. <i>Journal of Biological Chemistry</i> , 2002, 277, 45765-45769.	1.6	449
2	Support Vector Machines for Predicting Membrane Protein Types by Using Functional Domain Composition. <i>Biophysical Journal</i> , 2003, 84, 3257-3263.	0.2	307
3	Adaptive and freeze-tolerant heteronetwork organohydrogels with enhanced mechanical stability over a wide temperature range. <i>Nature Communications</i> , 2017, 8, 15911.	5.8	266
4	Predicting Drug-Target Interaction Networks Based on Functional Groups and Biological Features. <i>PLoS ONE</i> , 2010, 5, e9603.	1.1	241
5	Prediction of protein structural classes by support vector machines. <i>Computers & Chemistry</i> , 2002, 26, 293-296.	1.2	218
6	Prediction and analysis of essential genes using the enrichments of gene ontology and KEGG pathways. <i>PLoS ONE</i> , 2017, 12, e0184129.	1.1	202
7	Using LogitBoost classifier to predict protein structural classes. <i>Journal of Theoretical Biology</i> , 2006, 238, 172-176.	0.8	182
8	Predicting protein structural class by functional domain composition. <i>Biochemical and Biophysical Research Communications</i> , 2004, 321, 1007-1009.	1.0	176
9	Prediction of Membrane Protein Types by Incorporating Amphipathic Effects. <i>Journal of Chemical Information and Modeling</i> , 2005, 45, 407-413.	2.5	171
10	Prediction of protein subcellular locations by GO's FunD's PseAA predictor. <i>Biochemical and Biophysical Research Communications</i> , 2004, 320, 1236-1239.	1.0	165
11	Application of SVM to predict membrane protein types. <i>Journal of Theoretical Biology</i> , 2004, 226, 373-376.	0.8	164
12	Prediction of Antimicrobial Peptides Based on Sequence Alignment and Feature Selection Methods. <i>PLoS ONE</i> , 2011, 6, e18476.	1.1	164
13	Predicting Anatomical Therapeutic Chemical (ATC) Classification of Drugs by Integrating Chemical-Chemical Interactions and Similarities. <i>PLoS ONE</i> , 2012, 7, e35254.	1.1	159
14	Predicting Protein-Protein Interactions from Sequences in a Hybridization Space. <i>Journal of Proteome Research</i> , 2006, 5, 316-322.	1.8	158
15	Prediction and classification of protein subcellular location-sequence-order effect and pseudo amino acid composition. <i>Journal of Cellular Biochemistry</i> , 2003, 90, 1250-1260.	1.2	157
16	Identify Key Sequence Features to Improve CRISPR sgRNA Efficacy. <i>IEEE Access</i> , 2017, 5, 26582-26590.	2.6	153
17	Identification of Colorectal Cancer Related Genes with mRMR and Shortest Path in Protein-Protein Interaction Network. <i>PLoS ONE</i> , 2012, 7, e33393.	1.1	149
18	Support vector machines for predicting HIV protease cleavage sites in protein. <i>Journal of Computational Chemistry</i> , 2002, 23, 267-274.	1.5	145

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19	Predicting Functions of Proteins in Mouse Based on Weighted Protein-Protein Interaction Network and Protein Hybrid Properties. <i>PLoS ONE</i> , 2011, 6, e14556.	1.1	144
20	Predicting protein quaternary structure by pseudo amino acid composition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 282-289.	1.5	138
21	Support vector machines for predicting protein structural class. <i>BMC Bioinformatics</i> , 2001, 2, 3.	1.2	137
22	Gene expression differences among different MSI statuses in colorectal cancer. <i>International Journal of Cancer</i> , 2018, 143, 1731-1740.	2.3	137
23	Analysis of cancer-related lncRNAs using gene ontology and KEGG pathways. <i>Artificial Intelligence in Medicine</i> , 2017, 76, 27-36.	3.8	136
24	A new hybrid approach to predict subcellular localization of proteins by incorporating gene ontology. <i>Biochemical and Biophysical Research Communications</i> , 2003, 311, 743-747.	1.0	133
25	Support vector machines for predicting rRNA-, RNA-, and DNA-binding proteins from amino acid sequence. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003, 1648, 127-133.	1.1	131
26	Boosting classifier for predicting protein domain structural class. <i>Biochemical and Biophysical Research Communications</i> , 2005, 334, 213-217.	1.0	129
27	Prediction of lysine ubiquitination with mRMR feature selection and analysis. <i>Amino Acids</i> , 2012, 42, 1387-1395.	1.2	129
28	Analysis and Prediction of the Metabolic Stability of Proteins Based on Their Sequential Features, Subcellular Locations and Interaction Networks. <i>PLoS ONE</i> , 2010, 5, e10972.	1.1	123
29	Enantioselective Bromoaminocyclization of Allyl N-Tosylcarbamates Catalyzed by a Chiral Phosphine-Sc(OTf) ₃ Complex. <i>Journal of the American Chemical Society</i> , 2013, 135, 8101-8104.	6.6	117
30	Support vector machines for prediction of protein subcellular location by incorporating quasi-sequence-order effect. <i>Journal of Cellular Biochemistry</i> , 2002, 84, 343-348.	1.2	116
31	Predicting membrane protein type by functional domain composition and pseudo-amino acid composition. <i>Journal of Theoretical Biology</i> , 2006, 238, 395-400.	0.8	111
32	Predicting rRNA-, RNA-, and DNA-binding proteins from primary structure with support vector machines. <i>Journal of Theoretical Biology</i> , 2006, 240, 175-184.	0.8	111
33	Genetic differences among ethnic groups. <i>BMC Genomics</i> , 2015, 16, 1093.	1.2	109
34	Prediction of protein structural classes by neural network. <i>Biochimie</i> , 2000, 82, 783-785.	1.3	107
35	Nearest neighbour algorithm for predicting protein subcellular location by combining functional domain composition and pseudo-amino acid composition. <i>Biochemical and Biophysical Research Communications</i> , 2003, 305, 407-411.	1.0	107
36	Predicting protein localization in budding Yeast. <i>Bioinformatics</i> , 2005, 21, 944-950.	1.8	103

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37	Predicting Protein Structural Class with AdaBoost Learner. <i>Protein and Peptide Letters</i> , 2006, 13, 489-492.	0.4	103
38	Identification of synthetic lethality based on a functional network by using machine learning algorithms. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 405-416.	1.2	102
39	Predicting Enzyme Subclass by Functional Domain Composition and Pseudo Amino Acid Composition. <i>Journal of Proteome Research</i> , 2005, 4, 967-971.	1.8	96
40	Prediction of Protein-Protein Interaction Sites by Random Forest Algorithm with mRMR and IFS. <i>PLoS ONE</i> , 2012, 7, e43927.	1.1	92
41	Predicting enzyme family classes by hybridizing gene product composition and pseudo-amino acid composition. <i>Journal of Theoretical Biology</i> , 2005, 234, 145-149.	0.8	90
42	Support vector machines for prediction of protein signal sequences and their cleavage sites. <i>Peptides</i> , 2003, 24, 159-161.	1.2	89
43	Predicting subcellular localization of proteins in a hybridization space. <i>Bioinformatics</i> , 2004, 20, 1151-1156.	1.8	88
44	Predicting subcellular localization of proteins by hybridizing functional domain composition and pseudo-amino acid composition. <i>Journal of Cellular Biochemistry</i> , 2004, 91, 1197-1203.	1.2	88
45	Prediction of Protein Domain with mRMR Feature Selection and Analysis. <i>PLoS ONE</i> , 2012, 7, e39308.	1.1	86
46	Gene expression profiling gut microbiota in different races of humans. <i>Scientific Reports</i> , 2016, 6, 23075.	1.6	86
47	Classification and Analysis of Regulatory Pathways Using Graph Property, Biochemical and Physicochemical Property, and Functional Property. <i>PLoS ONE</i> , 2011, 6, e25297.	1.1	84
48	Predicting O-glycosylation sites in mammalian proteins by using SVMs. <i>Computational Biology and Chemistry</i> , 2006, 30, 203-208.	1.1	83
49	Identification of Differentially Expressed Genes between Original Breast Cancer and Xenograft Using Machine Learning Algorithms. <i>Genes</i> , 2018, 9, 155.	1.0	83
50	Artificial neural network model for predicting HIV protease cleavage sites in protein. <i>Advances in Engineering Software</i> , 1998, 29, 119-128.	1.8	81
51	Analysis and prediction of drug-drug interaction by minimum redundancy maximum relevance and incremental feature selection. <i>Journal of Biomolecular Structure and Dynamics</i> , 2017, 35, 312-329.	2.0	81
52	Identification of the copy number variant biomarkers for breast cancer subtypes. <i>Molecular Genetics and Genomics</i> , 2019, 294, 95-110.	1.0	81
53	Identification of gene expression signatures across different types of neural stem cells with the Monte Carlo feature selection method. <i>Journal of Cellular Biochemistry</i> , 2018, 119, 3394-3403.	1.2	78
54	Identify catalytic triads of serine hydrolases by support vector machines. <i>Journal of Theoretical Biology</i> , 2004, 228, 551-557.	0.8	77

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55	Prediction and analysis of cell-penetrating peptides using pseudo-amino acid composition and random forest models. <i>Amino Acids</i> , 2015, 47, 1485-1493.	1.2	77
56	Predicting enzyme family class in a hybridization space. <i>Protein Science</i> , 2008, 13, 2857-2863.	3.1	75
57	Predict and analyze S-nitrosylation modification sites with the mRMR and IFS approaches. <i>Journal of Proteomics</i> , 2012, 75, 1654-1665.	1.2	74
58	Identification of the Gene Expression Rules That Define the Subtypes in Glioma. <i>Journal of Clinical Medicine</i> , 2018, 7, 350.	1.0	74
59	Prediction of Pharmacological and Xenobiotic Responses to Drugs Based on Time Course Gene Expression Profiles. <i>PLoS ONE</i> , 2009, 4, e8126.	1.1	74
60	Support Vector Machine for predicting α -turn types. <i>Peptides</i> , 2003, 24, 629-630.	1.2	73
61	Prediction of protease types in a hybridization space. <i>Biochemical and Biophysical Research Communications</i> , 2006, 339, 1015-1020.	1.0	73
62	A hybrid method for prediction and repositioning of drug Anatomical Therapeutic Chemical classes. <i>Molecular BioSystems</i> , 2014, 10, 868.	2.9	70
63	Prediction of Deleterious Non-Synonymous SNPs Based on Protein Interaction Network and Hybrid Properties. <i>PLoS ONE</i> , 2010, 5, e11900.	1.1	70
64	Support vector machines for predicting the specificity of GalNAc-transferase. <i>Peptides</i> , 2002, 23, 205-208.	1.2	68
65	Deciphering the effects of gene deletion on yeast longevity using network and machine learning approaches. <i>Biochimie</i> , 2012, 94, 1017-1025.	1.3	67
66	Discriminating cirRNAs from other lncRNAs using a hierarchical extreme learning machine (H-ELM) algorithm with feature selection. <i>Molecular Genetics and Genomics</i> , 2018, 293, 137-149.	1.0	65
67	Identifying Patients with Atrioventricular Septal Defect in Down Syndrome Populations by Using Self-Normalizing Neural Networks and Feature Selection. <i>Genes</i> , 2018, 9, 208.	1.0	65
68	Support vector machines for the classification and prediction of β -turn types. <i>Journal of Peptide Science</i> , 2002, 8, 297-301.	0.8	64
69	Predicting protease types by hybridizing gene ontology and pseudo amino acid composition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 681-684.	1.5	64
70	Predicting Biological Functions of Compounds Based on Chemical-Chemical Interactions. <i>PLoS ONE</i> , 2011, 6, e29491.	1.1	64
71	Tissue Expression Difference between mRNAs and lncRNAs. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3416.	1.8	64
72	Prediction of protein-protein interactions based on PseAA composition and hybrid feature selection. <i>Biochemical and Biophysical Research Communications</i> , 2009, 380, 318-322.	1.0	62

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73	Identification of compound-protein interactions through the analysis of gene ontology, KEGG enrichment for proteins and molecular fragments of compounds. <i>Molecular Genetics and Genomics</i> , 2016, 291, 2065-2079.	1.0	62
74	Identification of leukemia stem cell expression signatures through Monte Carlo feature selection strategy and support vector machine. <i>Cancer Gene Therapy</i> , 2020, 27, 56-69.	2.2	62
75	Predicting the network of substrate-enzyme-product triads by combining compound similarity and functional domain composition. <i>BMC Bioinformatics</i> , 2010, 11, 293.	1.2	61
76	Tissue differences revealed by gene expression profiles of various cell lines. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 7068-7081.	1.2	59
77	Using AdaBoost for the prediction of subcellular location of prokaryotic and eukaryotic proteins. <i>Molecular Diversity</i> , 2008, 12, 41-45.	2.1	58
78	Classifying Ten Types of Major Cancers Based on Reverse Phase Protein Array Profiles. <i>PLoS ONE</i> , 2015, 10, e0123147.	1.1	58
79	Determining protein-protein functional associations by functional rules based on gene ontology and KEGG pathway. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140621.	1.1	58
80	Using Functional Domain Composition To Predict Enzyme Family Classes. <i>Journal of Proteome Research</i> , 2005, 4, 109-111.	1.8	57
81	Identifying Transcriptomic Signatures and Rules for SARS-CoV-2 Infection. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 627302.	1.8	57
82	Using GO-PseAA predictor to identify membrane proteins and their types. <i>Biochemical and Biophysical Research Communications</i> , 2005, 327, 845-847.	1.0	56
83	A novel computational method to predict transcription factor DNA binding preference. <i>Biochemical and Biophysical Research Communications</i> , 2006, 348, 1034-1037.	1.0	55
84	Using GO-PseAA predictor to predict enzyme sub-class. <i>Biochemical and Biophysical Research Communications</i> , 2004, 325, 506-509.	1.0	54
85	Predicting Subcellular Localization with AdaBoost Learner. <i>Protein and Peptide Letters</i> , 2008, 15, 286-289.	0.4	54
86	Signal Propagation in Protein Interaction Network during Colorectal Cancer Progression. <i>BioMed Research International</i> , 2013, 2013, 1-9.	0.9	53
87	Hepatitis C Virus Network Based Classification of Hepatocellular Cirrhosis and Carcinoma. <i>PLoS ONE</i> , 2012, 7, e34460.	1.1	52
88	Analysis and Prediction of Translation Rate Based on Sequence and Functional Features of the mRNA. <i>PLoS ONE</i> , 2011, 6, e16036.	1.1	51
89	Analysis and Prediction of Nitrated Tyrosine Sites with the mRMR Method and Support Vector Machine Algorithm. <i>Current Bioinformatics</i> , 2018, 13, 3-13.	0.7	51
90	Gene Ontology and KEGG Pathway Enrichment Analysis of a Drug Target-Based Classification System. <i>PLoS ONE</i> , 2015, 10, e0126492.	1.1	50

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91	Prediction of <i>Saccharomyces cerevisiae</i> protein functional class from functional domain composition. <i>Bioinformatics</i> , 2004, 20, 1292-1300.	1.8	49
92	Classification of Widely and Rarely Expressed Genes with Recurrent Neural Network. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 49-60.	1.9	49
93	Predicting Metabolic Pathways of Small Molecules and Enzymes Based on Interaction Information of Chemicals and Proteins. <i>PLoS ONE</i> , 2012, 7, e45944.	1.1	49
94	Identification of hepatocellular carcinoma related genes with k-th shortest paths in a protein-protein interaction network. <i>Molecular BioSystems</i> , 2013, 9, 2720.	2.9	47
95	Identifying and analyzing different cancer subtypes using RNA-seq data of blood platelets. <i>Oncotarget</i> , 2017, 8, 87494-87511.	0.8	47
96	Predicting 22 protein localizations in budding yeast. <i>Biochemical and Biophysical Research Communications</i> , 2004, 323, 425-428.	1.0	46
97	ECS: An automatic enzyme classifier based on functional domain composition. <i>Computational Biology and Chemistry</i> , 2007, 31, 226-232.	1.1	46
98	Computational prediction and analysis of protein $\hat{1}^3$ -carboxylation sites based on a random forest method. <i>Molecular BioSystems</i> , 2012, 8, 2946.	2.9	46
99	Predicting Protein Phenotypes Based on Protein-Protein Interaction Network. <i>PLoS ONE</i> , 2011, 6, e17668.	1.1	44
100	Analysis of Expression Pattern of snoRNAs in Different Cancer Types with Machine Learning Algorithms. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2185.	1.8	44
101	Identification of Protein Subcellular Localization With Network and Functional Embeddings. <i>Frontiers in Genetics</i> , 2020, 11, 626500.	1.1	44
102	Analysis of Tumor Suppressor Genes Based on Gene Ontology and the KEGG Pathway. <i>PLoS ONE</i> , 2014, 9, e107202.	1.1	44
103	Support Vector Machines for Prediction of Protein Domain Structural Class. <i>Journal of Theoretical Biology</i> , 2003, 221, 115-120.	0.8	43
104	A Novel Computational Approach To Predict Transcription Factor DNA Binding Preference. <i>Journal of Proteome Research</i> , 2009, 8, 999-1003.	1.8	41
105	Inferring Novel Tumor Suppressor Genes with a Protein-Protein Interaction Network and Network Diffusion Algorithms. <i>Molecular Therapy - Methods and Clinical Development</i> , 2018, 10, 57-67.	1.8	41
106	Prediction of Aptamer-Target Interacting Pairs with Pseudo-Amino Acid Composition. <i>PLoS ONE</i> , 2014, 9, e86729.	1.1	41
107	Prediction of Tyrosine Sulfation with mRMR Feature Selection and Analysis. <i>Journal of Proteome Research</i> , 2010, 9, 6490-6497.	1.8	40
108	Prediction of Body Fluids where Proteins are Secreted into Based on Protein Interaction Network. <i>PLoS ONE</i> , 2011, 6, e22989.	1.1	40

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109	Prediction of compoundsâ€™ biological function (metabolic pathways) based on functional group composition. <i>Molecular Diversity</i> , 2008, 12, 131-137.	2.1	39
110	HIV infection alters the human epigenetic landscape. <i>Gene Therapy</i> , 2019, 26, 29-39.	2.3	39
111	Multiple classifier integration for the prediction of protein structural classes. <i>Journal of Computational Chemistry</i> , 2009, 30, 2248-2254.	1.5	38
112	Prediction of Gene Phenotypes Based on GO and KEGG Pathway Enrichment Scores. <i>BioMed Research International</i> , 2013, 2013, 1-7.	0.9	38
113	Predicting Transcriptional Activity of Multiple Site p53 Mutants Based on Hybrid Properties. <i>PLoS ONE</i> , 2011, 6, e22940.	1.1	38
114	Predicting Heart Cell Types by Using Transcriptome Profiles and a Machine Learning Method. <i>Life</i> , 2022, 12, 228.	1.1	38
115	Is it a paradox or misinterpretation?. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 43, 336-338.	1.5	37
116	Prediction and analysis of protein palmitoylation sites. <i>Biochimie</i> , 2011, 93, 489-496.	1.3	37
117	Prediction of Protein Cleavage Site with Feature Selection by Random Forest. <i>PLoS ONE</i> , 2012, 7, e45854.	1.1	37
118	Predicting A-to-I RNA Editing by Feature Selection and Random Forest. <i>PLoS ONE</i> , 2014, 9, e110607.	1.1	37
119	Identifying Methylation Pattern and Genes Associated with Breast Cancer Subtypes. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4269.	1.8	37
120	Support Vector Machines for Prediction of Protein Subcellular Location. <i>Molecular Cell Biology Research Communications: MCBRC: Part B of Biochemical and Biophysical Research Communications</i> , 2000, 4, 230-233.	1.7	36
121	Classification of Non-Small Cell Lung Cancer Based on Copy Number Alterations. <i>PLoS ONE</i> , 2014, 9, e88300.	1.1	35
122	Prediction of subcellular protein localization based on functional domain composition. <i>Biochemical and Biophysical Research Communications</i> , 2007, 357, 366-370.	1.0	34
123	Identification of Genes Associated with Breast Cancer Metastasis to Bone on a Proteinâ€™Protein Interaction Network with a Shortest Path Algorithm. <i>Journal of Proteome Research</i> , 2017, 16, 1027-1038.	1.8	34
124	A method to distinguish between lysine acetylation and lysine ubiquitination with feature selection and analysis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2015, 33, 2479-2490.	2.0	33
125	Demonstration of two novel methods for predicting functional siRNA efficiency. <i>BMC Bioinformatics</i> , 2006, 7, 271.	1.2	32
126	Prediction of Protein Subcellular Locations with Feature Selection and Analysis. <i>Protein and Peptide Letters</i> , 2010, 17, 464-472.	0.4	32

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127	A computational method using the random walk with restart algorithm for identifying novel epigenetic factors. <i>Molecular Genetics and Genomics</i> , 2018, 293, 293-301.	1.0	32
128	Predicting RNA 5-Methylcytosine Sites by Using Essential Sequence Features and Distributions. <i>BioMed Research International</i> , 2022, 2022, 1-11.	0.9	32
129	Support vector machine for SAR/QSAR of phenethyl-amines. <i>Acta Pharmacologica Sinica</i> , 2007, 28, 1075-1086.	2.8	31
130	Prediction of active sites of enzymes by maximum relevance minimum redundancy (mRMR) feature selection. <i>Molecular BioSystems</i> , 2013, 9, 61-69.	2.9	31
131	Novel Candidate Key Drivers in the Integrative Network of Genes, MicroRNAs, Methylations, and Copy Number Variations in Squamous Cell Lung Carcinoma. <i>BioMed Research International</i> , 2015, 2015, 1-11.	0.9	31
132	Detecting the Multiomics Signatures of Factor-Specific Inflammatory Effects on Airway Smooth Muscles. <i>Frontiers in Genetics</i> , 2020, 11, 599970.	1.1	31
133	Finding Candidate Drugs for Hepatitis C Based on Chemical-Chemical and Chemical-Protein Interactions. <i>PLoS ONE</i> , 2014, 9, e107767.	1.1	31
134	Using Neural Networks for Prediction of Subcellular Location of Prokaryotic and Eukaryotic Proteins. <i>Molecular Cell Biology Research Communications: MCBRC: Part B of Biochemical and Biophysical Research Communications</i> , 2000, 4, 172-173.	1.7	30
135	Predicting N-terminal acetylation based on feature selection method. <i>Biochemical and Biophysical Research Communications</i> , 2008, 372, 862-865.	1.0	30
136	Prediction of Metabolic Pathway Using Graph Property, Chemical Functional Group and Chemical Structural Set. <i>Current Bioinformatics</i> , 2013, 8, 200-207.	0.7	30
137	Identification of new candidate drugs for lung cancer using chemical-chemical interactions, chemical-protein interactions and a K-means clustering algorithm. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 906-917.	2.0	30
138	Cancer-Related Triplets of mRNA-lncRNA-miRNA Revealed by Integrative Network in Uterine Corpus Endometrial Carcinoma. <i>BioMed Research International</i> , 2017, 2017, 1-7.	0.9	30
139	A novel approach to predict active sites of enzyme molecules. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 77-82.	1.5	29
140	Predicting the protein SUMO modification sites based on Properties Sequential Forward Selection (PSFS). <i>Biochemical and Biophysical Research Communications</i> , 2007, 358, 136-139.	1.0	29
141	A Comparison of Computational Methods for Identifying Virulence Factors. <i>PLoS ONE</i> , 2012, 7, e42517.	1.1	29
142	Prediction of Effective Drug Combinations by Chemical Interaction, Protein Interaction and Target Enrichment of KEGG Pathways. <i>BioMed Research International</i> , 2013, 2013, 1-10.	0.9	29
143	Data mining of the cancer-related lncRNAs GO terms and KEGG pathways by using mRMR method. <i>Mathematical Biosciences</i> , 2018, 304, 1-8.	0.9	29
144	Distinguishing Glioblastoma Subtypes by Methylation Signatures. <i>Frontiers in Genetics</i> , 2020, 11, 604336.	1.1	29

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145	Predicting Citrullination Sites in Protein Sequences Using mRMR Method and Random Forest Algorithm. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2017, 20, 164-173.	0.6	29
146	Prediction of Nitrated Tyrosine Residues in Protein Sequences by Extreme Learning Machine and Feature Selection Methods. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2018, 21, 393-402.	0.6	29
147	Artificial Neural Network Model for Predicting Membrane Protein Types. <i>Journal of Biomolecular Structure and Dynamics</i> , 2001, 18, 607-610.	2.0	28
148	Protein sumoylation sites prediction based on two-stage feature selection. <i>Molecular Diversity</i> , 2010, 14, 81-86.	2.1	28
149	Analysis of Protein Pathway Networks Using Hybrid Properties. <i>Molecules</i> , 2010, 15, 8177-8192.	1.7	28
150	Identification of retinoblastoma related genes with shortest path in a protein-protein interaction network. <i>Biochimie</i> , 2012, 94, 1910-1917.	1.3	28
151	An Information-Theoretic Machine Learning Approach to Expression QTL Analysis. <i>PLoS ONE</i> , 2013, 8, e67899.	1.1	28
152	Discriminating between deleterious and neutral non-frameshifting indels based on protein interaction networks and hybrid properties. <i>Molecular Genetics and Genomics</i> , 2015, 290, 343-352.	1.0	28
153	Identification of novel candidate drivers connecting different dysfunctional levels for lung adenocarcinoma using protein-protein interactions and a shortest path approach. <i>Scientific Reports</i> , 2016, 6, 29849.	1.6	28
154	Identification and analysis of the cleavage site in a signal peptide using SMOTE, dagging, and feature selection methods. <i>Molecular Omics</i> , 2018, 14, 64-73.	1.4	28
155	Investigating the gene expression profiles of cells in seven embryonic stages with machine learning algorithms. <i>Genomics</i> , 2020, 112, 2524-2534.	1.3	28
156	A Unified 35-Genes Signature for both Subtype Classification and Survival Prediction in Diffuse Large B-Cell Lymphomas. <i>PLoS ONE</i> , 2010, 5, e12726.	1.1	28
157	Artificial neural network model for predicting protein subcellular location. <i>Computers & Chemistry</i> , 2002, 26, 179-182.	1.2	27
158	Predicting Membrane Protein Types with Bagging Learner. <i>Protein and Peptide Letters</i> , 2008, 15, 590-594.	0.4	27
159	Identifying Protein Complexes Using Hybrid Properties. <i>Journal of Proteome Research</i> , 2009, 8, 5212-5218.	1.8	27
160	Prediction and analysis of protein methylarginine and methyllysine based on Multisequence features. <i>Biopolymers</i> , 2011, 95, 763-771.	1.2	27
161	Computational Analysis of HIV-1 Resistance Based on Gene Expression Profiles and the Virus-Host Interaction Network. <i>PLoS ONE</i> , 2011, 6, e17291.	1.1	27
162	Computational Methods for Protein-Protein Interaction and their Application. <i>Current Protein and Peptide Science</i> , 2005, 6, 443-449.	0.7	26

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163	Identification of Lung-Cancer-Related Genes with the Shortest Path Approach in a Protein-Protein Interaction Network. <i>BioMed Research International</i> , 2013, 2013, 1-8.	0.9	26
164	Identifying protein subcellular locations with embeddings-based node2loc. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	26
165	Operon prediction based on SVM. <i>Computational Biology and Chemistry</i> , 2006, 30, 233-240.	1.1	25
166	Prediction of Small Molecules Metabolic Pathways Based on Functional Group Composition. <i>Protein and Peptide Letters</i> , 2009, 16, 969-976.	0.4	25
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